

# Clustal W(1.4) multiple sequence alignment

4 Sequences Aligned. Alignment Score = 12736  
Gaps Inserted = 4 Conserved Identities = 308

Pairwise Alignment Mode: Slow  
Pairwise Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1 ..  
Similarity Matrix: blosum ..

FIGURE 1

Multiple Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1  
Delay Divergent = 40% Gap Distance = 8  
Similarity Matrix: blosum

Processing time: 14.5 seconds

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con3707.pep 1 MDQYCILGRIGEGAHGIVFKAHVPRVGVQCLPSILQTGEIVALKKVAL 50
con3705.pep 1 MDQYCILGRIGEGAHGIVFKAHVPRVGVQCLPSILQTGEIVALKKVAL 50
con3703.pep 1 MDQYCILGRIGEGAHGIVFKAHVET-----GEIVALKKVAL 37
con3702.pep 1 MDQYCILGRIGEGAHGIVFKAHVET-----GEIVALKKVAL 37
                *****
                *****

con3707.pep 51 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLS 100
con3705.pep 51 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLS 100
con3703.pep 38 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLS 87
con3702.pep 38 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLS 87
                *****

con3707.pep 101 LAEVRHAQRPLAQAVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 150
con3705.pep 101 LAEVRHAQRPLAQAVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 150
con3703.pep 88 LAEVRHAQRPLAQAVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 137
con3702.pep 88 LAEVRHAQRPLAQAVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 137
                *****

con3707.pep 151 SGQLKIADFGRLARVSPDGSRLYTHQVATRWYRAPELLYGARQYDQGV 200
con3705.pep 151 SGQLKIADFGRLARVSPDGSRLYTHQVATRWYRAPELLYGARQYDQGV 200
con3703.pep 138 SGQLKIADFGRLARVSPDGSRLYTHQVATR----- 167
con3702.pep 138 SGQLKIADFGRLARVSPDGSRLYTHQVATRWYRAPELLYGARQYDQGV 187
                *****

con3707.pep 201 WSVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWPELTELDPY 250
con3705.pep 201 WSVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWP----- 242
con3703.pep 168 -SVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWPELTELDPY 216
con3702.pep 188 WSVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWPELTELDPY 237
                *****

con3707.pep 251 NKISFKEQVPMPLVEVLDPVSPQALDLLGQFLLYPPHQRIAASKALLHQY 300
con3705.pep 243 -----EQVPMPLVEVLDPVSPQALDLLGQFLLYPPHQRIAASKALLHQY 286
con3703.pep 217 NKISLKEQVPMPLVEVLDPVSPQALDLLGQFLLYPPHQRIAASKALLHQY 266
con3702.pep 238 NKISFKEQVPMPLVEVLDPVSPQALDLLGQFLLYPPHQRIAASKALLHQY 287
                *****

con3707.pep 301 FFTAPLPAHPSELVPPQRLGGPAPKAHPGPPHIHDFHVDRLPLEESLLNPE 350
con3705.pep 287 FFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRLPLEESLLNPE 336
con3703.pep 267 FFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRLPLEESLLNPE 316
con3702.pep 288 FFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRLPLEESLLNPE 337
                *****

con3707.pep 351 LIRPFILEG 359
con3705.pep 337 LIRPFILEG 345
con3703.pep 317 LIRPFILER 325
con3702.pep 338 LIRPFILER 346
                *****

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# Clustal W(1.4) multiple sequence alignment

4 Sequences Aligned. Alignment Score = 42511  
Gaps Inserted = 4 Conserved Identities = 932

Pairwise Alignment Mode: Slow  
Pairwise Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 5.0

Multiple Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 5.0  
Delay Divergent = 40% Transitions: Weighted

Processing time: 107.3 seconds

FIGURE 2

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con3702.seq      1      ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG      38
con3703.seq      1 GGACCTTCTAGAAATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG      50
con3707.seq      1      ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG      38
con3705.seq      1      ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG      38
                    *****

con3702.seq      39 CGCCACACGGCATCGTCTTCAAGGCCAAGCACGTGGAG-----      75
con3703.seq      51 CGCCACACGGCATCGTCTTCAAGGCCAAGCACGTGGAG-----      87
con3707.seq      39 CGCCACACGGCATCGTCTTCAAGGCCAAGCACGTGGAGCCGAGGGTGGGCT      88
con3705.seq      39 CGCCACACGGCATCGTCTTCAAGGCCAAGCACGTGGAGCCGAGGGTGGGCT      88
                    *****

con3702.seq      76 -----ACTGGCGAGATAGTTGCCCTCAAG      99
con3703.seq      88 -----ACTGGCGAGATAGTTGCCCTCAAG      111
con3707.seq      89 GGCAGTGTCTGCCTTCTATCCTGCAGACTGGCGAGATAGTTGCCCTCAAG      138
con3705.seq      89 GGCAGTGTCTGCCTTCTATCCTGCAGACTGGCGAGATAGTTGCCCTCAAG      138
                    *****

con3702.seq      100 AAGGTGGCCCTAAGGCGGTTGGAAGACGGCTTCCCTAACCAGGCCCTGCG      149
con3703.seq      112 AAGGTGGCCCTAAGGCGGTTGGAAGACGGCTTCCCTAACCAGGCCCTGCG      161
con3707.seq      139 AAGGTGGCCCTAAGGCGGTTGGAAGACGGCTTCCCTAACCAGGCCCTGCG      188
con3705.seq      139 AAGGTGGCCCTAAGGCGGTTGGAAGACGGCTTCCCTAACCAGGCCCTGCG      188
                    *****

con3702.seq      150 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC      199
con3703.seq      162 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC      211
con3707.seq      189 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC      238
con3705.seq      189 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC      238
                    *****

con3702.seq      200 TGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC      249
con3703.seq      212 TGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC      261
con3707.seq      239 TGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC      288
con3705.seq      239 TGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC      288
                    *****

con3702.seq      250 ATGCTGTTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGC      299
con3703.seq      262 ATGCTGTTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGC      311
con3707.seq      289 ATGCTGTTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGC      338
con3705.seq      289 ATGCTGTTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGC      338
                    *****

con3702.seq      300 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCGCCT      349
con3703.seq      312 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCGCCT      361
con3707.seq      339 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCGCCT      388
con3705.seq      339 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCGCCT      388

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(FIGURE 2, cont)

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*****
con3702.seq 350 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG 399
con3703.seq 362 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG 411
con3707.seq 389 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG 438
con3705.seq 389 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG 438
*****
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con3702.seq 400 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG 449
con3703.seq 412 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG 461
con3707.seq 439 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG 488
con3705.seq 439 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG 488
*****
con3702.seq 450 AGTCTTTTCCCCAGACGGCAGCCGCCCTCTACACACACCAGGTGGCCACCA 499
con3703.seq 462 AGTCTTTTCCCCAGACGGCAGCCGCCCTCTACACACACCAGGTGGCCACCA 511
con3707.seq 489 AGTCTTTTCCCCAGACGGCAGCCGCCCTCTACACACACCAGGTGGCCACCA 538
con3705.seq 489 AGTCTTTTCCCCAGACGGCAGCCGCCCTCTACACACACCAGGTGGCCACCA 538
*****
con3702.seq 500 GGTGGTACCGAGCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG 549
con3703.seq 512 GGT----- 514
con3707.seq 539 GGTGGTACCGAGCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG 588
con3705.seq 539 GGTGGTACCGAGCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG 588
***
con3702.seq 550 GCGTCGATCTGTGGTCTGTGGGCTGCATCATGGGGAGCTGTTGAATGG 599
con3703.seq 515 -----CTGTGGGCTGCATCATGGGGAGCTGTTGAATGG 548
con3707.seq 589 GCGTCGATCTGTGGTCTGTGGGCTGCATCATGGGGAGCTGTTGAATGG 638
con3705.seq 589 GCGTCGATCTGTGGTCTGTGGGCTGCATCATGGGGAGCTGTTGAATGG 638
*****
con3702.seq 600 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC 649
con3703.seq 549 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC 598
con3707.seq 639 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC 688
con3705.seq 639 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC 688
*****
con3702.seq 650 TTCGCATCTTGGGCACCCCAAACCCCTCAAGTCTGGCCGGAGCTCACTGAG 699
con3703.seq 599 TTCGCATCTTGGGCACCCCAAACCCCTCAAGTCTGGCCGGAGCTCACTGAG 648
con3707.seq 689 TTCGCATCTTGGGCACCCCAAACCCCTCAAGTCTGGCCGGAGCTCACTGAG 738
con3705.seq 689 TTCGCATCTTGGGCACCCCAAACCCCTCAAGTCTGGCCGGAGC----- 730
*****
con3702.seq 700 CTGCCGGACTACAACAAGATCTCCTTTAAGGAGCAGGTGCCCATGCCCCT 749
con3703.seq 649 CTGCCGGACTACAACAAGATCTCCTTTAAGGAGCAGGTGCCCATGCCCCT 698
con3707.seq 739 CTGCCGGACTACAACAAGATCTCCTTTAAGGAGCAGGTGCCCATGCCCCT 788
con3705.seq 731 -----AGGTGCCCATGCCCCT 746
*****
con3702.seq 750 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC 799
con3703.seq 699 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC 748
con3707.seq 789 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC 838
con3705.seq 747 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC 796
*****
con3702.seq 800 AATTCCTTCTCTACCCCTCCTACCAGCGCATCGCAGCTTCCAAGGCTCTC 849
con3703.seq 749 AATTCCTTCTCTACCCCTCCTACCAGCGCATCGCAGCTTCCAAGGCTCTC 798
con3707.seq 839 AATTCCTTCTCTACCCCTCCTACCAGCGCATCGCAGCTTCCAAGGCTCTC 888
con3705.seq 797 AATTCCTTCTCTACCCCTCCTACCAGCGCATCGCAGCTTCCAAGGCTCTC 846
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(FIGURE 2 cont)

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con3702.seq 850 CTCCATCAGTACTTCTTCACAGCTCCCCCTGCCTGCCCCATCCATCTGAGCT 899
con3703.seq 799 CTCCATCAGTACTTCTTCACAGCTCCCCCTGCCTGCCCCATCCATCTGAGCT 848
con3707.seq 889 CTCCATCAGTACTTCTTCACAGCTCCCCCTGCCTGCCCCATCCATCTGAGCT 938
con3705.seq 847 CTCCATCAGTACTTCTTCACAGCTCCCCCTGCCTGCCCCATCCATCTGAGCT 896
*****

con3702.seq 900 GCCGATTCTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC 949
con3703.seq 849 GCCGATTCTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC 898
con3707.seq 939 GCCGGTTCTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC 988
con3705.seq 897 GCCGATTCTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC 946
*****

con3702.seq 950 CCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG 999
con3703.seq 899 CCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG 948
con3707.seq 989 CCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG 1038
con3705.seq 947 CCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG 996
*****

con3702.seq 1000 TTGAACCCAGAGCTGATTTCGGCCCTTCATCCTGGAGGGGTGAGGATCCTG 1049
con3703.seq 949 TTGAACCCAGAGCTGATTTCGGCCCTTCATCCTGGAGAGGTGAGGATCCTG 998
con3707.seq 1039 TTGAACCCAGAGCTGATTTCGGCCCTTCATCCTGGAGGGGTGAGGATCCTG 1088
con3705.seq 997 TTGAACCCAGAGCTGATTTCGGCCCTTCATCCTGGAGGGGTGA 1038
*****

con3702.seq 1050 AGAA 1053
con3703.seq 999 AGAA 1002
con3707.seq 1089 AGAA 1092
con3705.seq 1039 1038

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